NRi research highlights

Swine Radiation Hybrid Map Helps to Reveal Important Traits

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Over the past 5 years swine researchers have developed more than 1,000 DNA-based markers that have been used to establish genetic linkage maps for the swine genome.

These linkage maps provide the basis for detection of chromosomal regions containing genes that contribute to important economic trait loci (ETL) in swine – such as growth, reproductive capacity, and carcass quality.

Although current genetic maps have sufficient markers to detect ETL, they lack the resolution necessary to identify the actual genes contributing to these traits or to distinguish which individual animals carry them. Additional genetic markers are needed to identify these ETLs.
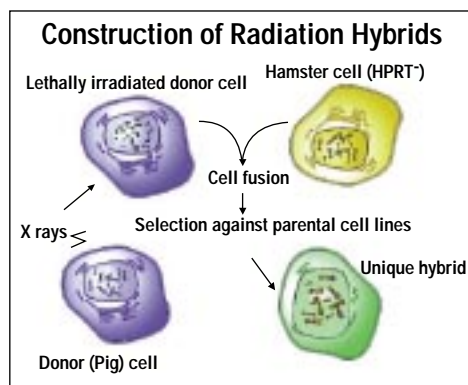
Furthermore, genetic maps with higher resolution are needed to facilitate comparative mapping between the human and swine genomes. Comparative mapping allows the transfer of genetic knowledge from species such as humans – for which extensive research has identified the sequence and location of thousands of genes – to a species such as swine where gene identification is not as far advanced.

Radiation hybrid (RH) mapping is an important research tool that provides an opportunity to incorporate anonymous markers such as microsatellites (short tracts of repeated deoxyribonucleic acid or DNA), as well as genes or pieces of genes (expressed sequence tags or ESTs that could be obtained from the genome of other species) onto a single gene map. As a result, RH maps can be used to identify genes regulating economic traits of interest.

SWINE GENE MAPPING

USDA's National Research Initiative Competitive Grants Program has supported research aimed at developing genetic markers and genetic maps for the swine genome. With NRI support, researchers at

FLOWCHART INDICATING THE PROCEDURE TO PRODUCE RADIATION HYBRIDS.
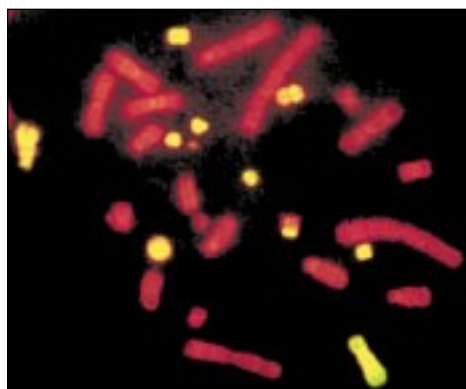

Construction of Radiation Hybrids

Lethally irradiated donor cell

Hamster cell (HPRT⁻)

Cell fusion

X rays

Selection against parental cell lines

Unique hybrid

Donor (Pig) cell

the Program in Comparative Genomics, University of Minnesota, in collaboration with researchers at the Laboratoire de Génétique Cellulaire, INRA, Toulouse, France, have cooperated in an effort to build a high-resolution RH map for the swine genome. These research tools are currently used around the world to identify ETL in swine.

Radiation hybrids were produced by joining lethally irradiated donor cells (pig cell line) with recipient cells (hamster cell line) (front page) to produce a hybrid that contains a full complement of recipient chromosomes, and pieces of donor chromosomes (which were fragmented by the irradiation process) (below).

A total of 118 unique hybrids were produced (INRA-University of Minnesota porcine Radiation Hybrid or IMpRH panel*), which contain all parts of the swine genome. DNA from each hybrid in this panel was then used to amplify 757 markers via the polymerase chain reac-

tion (PCR). The marker retention pattern of each hybrid was assessed and a radiation hybrid map produced for each swine chromosome.

IMPACT

The researchers have successfully created a high-resolution swine RH map – critical to identifying physical regions of the swine genome containing ETLs – and demonstrated the ease of mapping genes, expressed sequence tags, and anonymous random markers such as microsatellites on a single map.

This research tool enables specific regions of the swine genome to be targeted for the addition of new informative markers. This capability is imperative to fine-mapping ETL and positional candidate cloning in the swine genome.

This map serves as a template or blueprint indicating the order of DNA sequences in the genome of any species. This knowledge is key to manipulating livestock genomes through marker-assisted selection, which is critical to improved livestock production and sustaining agriculture in the new century. ❖

DETECTION OF SWINE DNA IN THE RECIPIENT HAMSTER CELL LINE. THE YELLOW FLUORESCENCE INDICATES AREAS OF THE HAMSTER CHROMOSOMES WHERE SWINE DNA HAS BEEN INCORPORATED.

MARTINE YERLE

Besides L. Schook, other researchers on this project include R. Hawken, L. Alexander, and C. Beattie, University of Minnesota; and M. Yerle, J. Gellin, and D. Milan, Laboratoire de Génétique Cellulaire, INRA, Toulouse, France.